

GenCore version 4.5
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v .

OM protein - protein search, using sw model.

Run on: September 4, 2002, 16:13:06 ; Search time 101.54 Seconds

(without alignments)
48.262 Million cell updates/sec

Title: US-09-052-089A-6

Sequence: 1 LSQCTICSDFFDHSDVAI.....IOWFETAPSRTCPQCRIQVG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	244	83.3	433	T30807
2	127	43.3	310	C84701
3	125	42.7	325	T86321
4	123	42.0	158	T13738
5	113	38.6	224	E86321
6	112	38.2	344	T05064
7	110	37.5	274	T48296
8	108	36.9	489	T26069
9	107	36.5	137	T46904
10	107	36.5	551	S6695
11	106.5	36.3	506	F85016
12	106.5	36.3	2	H9674
13	106	36.2	425	T25457
14	106	36.2	524	F96572
15	106	36.2	1238	T15919
16	105	35.8	2	F7125
17	104.5	35.7	441	2
18	104	35.5	351	2
19	102.5	35.5	2	G84678
20	102	34.8	190	2
21	102	34.8	292	T06684
22	101.5	34.6	425	2
23	100.5	34.3	157	2
24	100.5	34.3	157	2
25	99.5	34.0	206	2
26	99.5	34.0	1610	2
27	98.5	33.6	227	2
28	98	33.4	204	2
29	98	33.4	2	G84530

RESULT	Match	Query	Match	Length	DB	ID	Description
1	T0807	TRAF interacting protein	Pugu rubripes	83.0%	Best Local Matches	39;	TRAF interacting protein - Pugu rubripes
2	C84701	hypothetical protein	C;Species: Pugu rubripes	39;	Conservative	6;	C;Species: Pugu rubripes
3	T86321	F6114.12 protein -	C;Accession: T30807	39;	Mismatches	2;	C;Accession: T30807
4	T13738	hypothetical protein	R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheeler, D.; Bishop, M.; Elgar, FEB5 Leftt, 443, 370-374, 1999	39;	Indels	0;	R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheeler, D.; Bishop, M.; Elgar, FEB5 Leftt, 443, 370-374, 1999
5	E86321	hypothetical protein	A;Title: Three receptor genes for plasminogen related growth factors in the genome of	39;	Gaps	0;	A;Title: Three receptor genes for plasminogen related growth factors in the genome of
6	T05064	hypothetical protein	A;Reference number: Z20880; MUID:99148833	39;			A;Reference number: Z20880; MUID:99148833
7	A86315	hypothetical protein	A;Accession: T30807	39;			A;Accession: T30807
8	T48296	hypothetical protein	A;Status: preliminary; translated from GB/EMBL/DDJB	39;			A;Status: preliminary; translated from GB/EMBL/DDJB
9	T26069	hypothetical protein	A;Molecule type: DNA	39;			A;Molecule type: DNA
10	A86321	hypothetical protein	A;Residues: 1-433 <COT>	39;			A;Residues: 1-433 <COT>
11	T46904	hypothetical protein	A;Cross-references: EMBL:AJ010317; NID:e1355235; PIDN:CAA09084.1	39;			A;Cross-references: EMBL:AJ010317; NID:e1355235; PIDN:CAA09084.1
12	F7125	hypothetical protein	C;Genetics:	39;			C;Genetics:
13	2	hypothetical protein	A;Gene: TRIP	39;			A;Gene: TRIP
14	2	hypothetical protein	A;Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3	39;			A;Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

ALIGNMENTS

Query	Match	Best Local Simililarity	83.0%	Score	244	DB	2	Length	433;	
Qy	Db	39;	Conservative	6;	Mismatches	2;	Indels	0;	Gaps	0;
C84701	7	CTICSDFFDHSDVAI	CTICSDFFDHSDVAI	50	50	50	50	50	50	50
		HQGHTPHLQLQI	HQGHTPHLQLQI							
		WETAPSRTCPQCRIQV	WETAPSRTCPQCRIQV							
		53	CTICSDFFDHSDVAI	HQGHTPHLQLQI	WETAPSRTCPQCRIQV	53				

RESULT	Match	Query	Match	Length	DB	ID	Description
1	C84701	hypothetical protein At2g29840 [imported] - Arabidopsis thaliana (mouse-ear cress)	C;Species: Arabidopsis thaliana (mouse-ear cress)	83.0%	Best Local Matches	39;	hypothetical protein At2g29840 [imported] - Arabidopsis thaliana (mouse-ear cress)
2		C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001	39;	Conservative	6;	C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
3		C;Accession: C84701	C;Accession: C84701	39;	Mismatches	2;	C;Accession: C84701
4		R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature, 402, 761-768, 1999	R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature, 402, 761-768, 1999	39;	Indels	0;	R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.C.D.; Fujii, C.Y.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature, 402, 761-768, 1999
5		A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.	39;	Gaps	0;	A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
6		A;Reference number: A84420; MUID:20083487	A;Reference number: A84420; MUID:20083487	39;			A;Reference number: A84420; MUID:20083487
7		A;Accession: C84701	A;Accession: C84701	39;			A;Accession: C84701
8		A;Status: preliminary	A;Status: preliminary	39;			A;Status: preliminary
9		A;Molecule type: DNA	A;Molecule type: DNA	39;			A;Molecule type: DNA
10		A;Residues: 1-310 <STO>	A;Residues: 1-310 <STO>	39;			A;Residues: 1-310 <STO>
11		A;Cross-references: GB:AE002093; NID:g3582320; PIDN:AAC35217.1; GSDB:GN00139	A;Cross-references: GB:AE002093; NID:g3582320; PIDN:AAC35217.1; GSDB:GN00139	39;			A;Cross-references: GB:AE002093; NID:g3582320; PIDN:AAC35217.1; GSDB:GN00139
12		C;Genetics:	C;Genetics:	39;			C;Genetics:
13		A;Gene: At2g29840	A;Gene: At2g29840	39;			A;Gene: At2g29840
14		A;Map position: 2	A;Map position: 2	39;			A;Map position: 2
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16				39;			
17				39;			
18				39;			
19				39;			
20				39;			
21				39;			
22				39;			
23				39;			
24				39;			
25				39;			
26				39;			
27				39;			
28				39;			
29				39;			
30				39;			
31				39;			
32				39;			
33				39;			
34				39;			
35				39;			
36				39;			
37				39;			
38				39;			
39				39;			
40				39;			
41				39;			
42				39;			
43				39;			
44				39;			
45				39;			

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C;Accession:	F86321												C; Accession: E86321
R: Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, R.; ansen, N.F.; Hughes, B.; Huizar, L.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Aker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Nature 408, 816-820, 2000													
A;Authors:	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, C.A.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719												
A;Accession:	F86321												A; Accession: E86321
A;Status: preliminary													A; Status: preliminary
A;Molecule type: DNA													A; Molecule type: DNA
A;Residues: 1-325 <STO>													A; Residues: 1-325 <STO>
A;Cross-references: GB:AE005172; PIDN:AAF27102.1; GSPDB:GN00141													A; Cross-references: GB:AE005172; PIDN:AAF27102.1; GSPDB:GN00141
C;Genetics:													C; Genetics:
A;Map position: 1													A; Map position: 1
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Matches	19;	Conservative	11;	Mismatches	16;	Indels	2;	Gaps	1;				Indels
RESULT	4												
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Matches	19;	Conservative	11;	Mismatches	16;	Indels	2;	Gaps	1;				Indels
RESULT	4												
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RESULT	4												
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Matches	19;	Conservative	11;	Mismatches	16;	Indels	2;	Gaps	1;				Indels
RESULT	4												
Qy	3	LCTICSDFFDHRSRVAIAHCGHTFHQLQCLQWTFETAPSRCPOCRIQV	50										Query Match
Db	276	VCTICLEEFDGSRIVTLPKGHEFDDECVIEWF--VRSHVCPCLRIEL	321										Best Local Similarity
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RESULT	4												
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RESULT	4												
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, M.C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Aasen, N.F.; Hughes, B.; Huijzer, L.
Nature 408, 816-820, 2000
 A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luhrs, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A; Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A; Reference number: A86141; MUID:21016719
 A; Accession: A8615
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-383 <STO>
 A; Cross-references: GB:AE005172; NID:99665074; PIBN:AAF97276.1; GSPDB:GN00141
 C; Genetics:
 A; Map position: 1

CESP:W02A11.3

```

Query Match          38.2%;  Score 112;  DB 2;  Length 383;
Best Local Similarity 36.4%;  Pred. No. 8-06; 保守的 11;  Mismatches 15;  Indels 2;  Gaps 1;
Matches 16;  Conservative 11;  Mismatches 15;  Indels 2;  Gaps 1;

Qy      4 CTICSDFFDHRSRVAIHCQHTFHQLCIIQWFETAPSRTCPQR 47
Db      335 CSICQDEVEREDEVGELNCQGHSPHVHCVKQWL--SRKNACPVC 376

RESULT          8
T48296
hypothetical protein F9G14_60 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
C;Accession: T48296
R;Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; Deewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24491
A;accession: T48296
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <BEV>
A;Cross-references: EMBL:ALI62973
A;Experimental source: cultivar Columbia; BAC clone F9G14
C;Genetics:
A;Map position: 5
A;Note: F9G14_60
C;superfamily: RING finger homology <RRN>
F;201-251/Domain: RING finger homology <RRN>

Query Match          37.5%;  Score 110;  DB 2;  Length 274;
Best Local Similarity 39.3%;  Pred. NO. 1e-05; 保守的 18;  Mismatches 20;  Indels 7;  Gaps 2;
Matches 18;  Conservative 7;  Mismatches 20;  Indels 2;  Gaps 1;
Oy      4 CTICSDFFDHRSRVAIHCQHTFHQLCIIQWFETAPSRTCPQRIV 50
Db      205 CVCICKEEMSEGRDVCMPQHFFHWKCILPWL--SKKNCPFCRFQL 249

RESULT          9
T26069
hypothetical protein W02A11_3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T26069
R:white, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20147
A;accession: T26069
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA

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Query Match	Score	DB	Length
Best Local Similarity	Pred. No.	DB-05;	137:
Matches	Mismatches	Indels	Gaps
OY	4	CTICSDFFDHSRDOVAATHCGHTFHLOCLIQETAPSRCPOCRIQV	50
Db	85	CTICLISLEEGEDVRRFLPCMHFLHQVQYDQWLIT--NKKCPICRVDI	129
RESULT	11		
S66695			
probable membrane protein YOL013c - yeast (Saccharomyces cerevisiae)			
N;Alternate names: hypothetical protein o2341			
C;Species: Saccharomyces cerevisiae			
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 02-Sep-2000			
C;Accession: S66695			
R;Hughes, B.; Pohl, T.M.			
R;submitted to the Protein Sequence Database, July 1996			
A;Reference number: S66685			
A;Accession: S66695			
A;Molecule type: DNA			
A;Residues: 1-551 <HUG>			
A;Cross-references: EMBL:274755; NID:91419784; PID:e252259; PID:91419785; MIPS:YOL013C			
A;Experimental source: strain S288C			
C;Genetics:			
A;Gene: SGD:HRD1			
A;Cross-references: SSD:00005373; MIPS:YOL013C			
A;Map position: 15L			
C;Superfamily: RING finger homology			
C;Keywords: transmembrane protein			
F:10-26;Domain: transmembrane #status predicted <TM1>			
F:46-62;Domain: transmembrane #status predicted <TM2>			

Query Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps	1;
F;05-121/Domain: transmembrane #status predicted <TM3> F;14-160/Domain: transmembrane #status predicted <TM4> F;345-405/Domain: RING finger homology <RRN>									
Query Match	36.5%	Score 107;	DB 2;	Length 551;					
Best Local Similarity	37.3%	Pred. No.	4.3e-05;						
Matches	22;	Conservative	6;	Mismatches	19;	Indels	12;	Gaps	2;
Qy	2 SLCTICSDPFDHS-----RDVAIHCIGTFHLQCLIONFETAPSRTCPQCRIQV 50	Db	347 NCICICMDELHSPNQQTWKNNKKPKRULPCGHTLHSCLKNNMER--SQTCPICRLPV 403						
RESULT 12									
F85016 probable RING zinc finger protein [imported] - Arabidopsis thaliana									
C;Species: Arabidopsis thaliana (mouse-ear cress)									
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001									
C;Accession: F85016									
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999									
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.									
A;Reference number: A85001; MUID: 20083488									
A;Accession: F85016									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-506 <STO>									
A;Cross-references: GB:NC_001268; NID:97267624; PIDN:CA80936.1; GSPDB:GN00140									
C;Genetics:									
C;Gene: AT4g01270									
A;Map position: 4									
Query Match	36.3%	Score 106.5;	DB	2;	Length 506;				
Best Local Similarity	39.6%	Pred. No.	4.5e-05;						
Matches	21;	Conservative	10;	Mismatches	13;	Indels	9;	Gaps	3;
Qy	2 SLCTICSDPFDHSRDAVAAHCIGTFHLQCLIONFETAPSRTCPQCRIQV 47	Db	10 AICISCYEDLKPVENLQSIKA-CGHVFHELLQWFEYCPSSTNKRNCPICK 60						
RESULT 13									
H9764 protein RING zinc finger protein F25P22.18 [imported] - Arabidopsis thaliana									
C;Species: Arabidopsis thaliana (mouse-ear cress)									
C;Accession: H9764									
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001									
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.									
Nature 408, 816-820, 2000									
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.									
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.									
A;Reference number: A86141; MUID: 21016719									
A;Accession: H9764									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-367 <STO>									
A;Cross-references: GB:AE005173; NID:96692739; PIDN:AAF24845.1; GSPDB:GN00141									
C;Genetics:									
C;Gene: F25P22.18									
A;Map position: 1									
Query Match	36.2%	Score 106;	DB	2;	Length 524;				
Best Local Similarity	36.4%	Pred. No.	4e-05;						
Matches	16;	Conservative	8;	Mismatches	18;	Indels	2;	Gaps	1;
Qy	4 CTTCSDPFDHSRDAVAAHCIGTFHLQCLIONFETAPSRTCPQCRIQV 47	Db	319 CTCQDEYEAKDEVGEILRGRHRHFRIDCVNNQWL-VRKNSCPCK 360						
RESULT 14									
T22457 hypothetical protein B0432.9 - Caenorhabditis elegans									
C;Species: Caenorhabditis elegans									
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000									
R;Henkhaus, J.; Wohlmann, P. submitted to the EMBL Data Library, December 1996									
A;Description: The sequence of C. elegans cosmid B0432.									
A;Reference number: Z220038									
A;Accession: T25457									
A;Status: preliminary; translated from GB/EMBL/DDBj									
A;Molecule type: DNA									
A;Residues: 1-425 <HEN>									
A;Cross-references: EMBL:UB0836; PIDN:AB37893.1; GSPDB:GN00020; CESP:B0432.9									
A;Experimental source: strain Bristol N2; clone B0432									
A;Gene: CESP:B0432.9									
A;Map position: 2									
A;Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2									
C;Superfamily: RING finger homology									
F;188-238/Domain: RING finger homology <RRN>									
Query Match	36.2%	Score 106;	DB	2;	Length 425;				
Best Local Similarity	40.9%	Pred. No.	4.5e-05;						
Matches	18;	Conservative	7;	Mismatches	17;	Indels	2;	Gaps	1;
Qy	4 CTTCSDPFDHSRDAVAAHCIGTFHLQCLIONFETAPSRTCPQCRIQV 47	Db	192 CSICFEDLQNDKISAVCIGHYHGCISOWIA-KRCPCSCR 233						
RESULT 15									
F9572 protein F12M16.10 [imported] - Arabidopsis thaliana									
C;Species: Arabidopsis thaliana (mouse-ear cress)									
C;Accession: F9572									
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.									
Nature 408, 816-820, 2000									
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Taloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.									
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.									
A;Reference number: A86141; MUID: 21016719									
A;Accession: F9572									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-524 <STO>									
A;Cross-references: GB:AE005173; NID:97769853; PIDN:AAF69531.1; GSPDB:GN00141									
C;Genetics:									
C;Gene: F12M16.10									
A;Map position: 1									
Query Match	36.2%	Score 106;	DB	2;	Length 524;				
Best Local Similarity	36.4%	Pred. No.	4e-05;						
Matches	16;	Conservative	8;	Mismatches	18;	Indels	2;	Gaps	1;
Qy	4 CTTCSDPFDHSRDAVAAHCIGTFHLQCLIONFETAPSRTCPQCRIQV 47	Db	319 CTCQDEYEAKDEVGEILRGRHRHFRIDCVNNQWL-VRKNSCPCK 360						

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: AB5001; MUID: 20083488
A;Accession: C85067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Cross-references: GB:NC_001268; NID:97267295; PIDN:CAB81077.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g05350
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING fi

Query Match 34.0%; Score 99.5; DB 2; Length 206;
Best Local Similarity 36.0%; Pred. No. 0.00014; Matches 18; Conservative 8; Mismatches 19; Indels 5; Gaps 2; Db 157 CSICLESLVSGPKPRDVTMTCSSHVFHNGCLLWLR--KNTCPLCRTE 204

RESULT 26

T11681 hypothetical protein SPBC21D10.09c - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C;Accession: T11681
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, September 1998
A;Reference number: Z17313
A;Accession: T11681
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-1610 <SEE>
A;Cross-references: EML:AL031536; NID:e1319499; PID:e1319508
A;Experimental source: strain 97h(-)
C;Genetics:
A;Map position: IIR
A;Introns: 10/2
A;Note: SPBC21D10.09c
C;Superfamily: RING finger homology homology <RRN>
F;1554-1609/Domain: RING finger homology <RRN>

Query Match 34.0%; Score 99.5; DB 2; Length 1610;
Best Local Similarity 38.3%; Pred. No. 0.00082; Matches 18; Conservative 5; Mismatches 21; Indels 3; Gaps 1; Db 1558 CAICYSVLSVERTLPNKRGTCRHKFHASCYKWFKSSNNSSRCPLCR 1604

RESULT 27

T00428 hypothetical protein At2g47560 [imported] - Arabidopsis thaliana
N;Alternative names: hypothetical protein T30B22.14
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00428; G49156
R;Rounseley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
submitted to the EMBL Data Library, October 1998 BAC T30B22 genomic sequence.
A;Descriptor: *Arabidopsis thaliana* chromosome 11 BAC T30B22 genomic sequence.
A;Reference number: Z14149
A;Accession: T00428
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-227 <ROU>
A;Cross-references: EMBL:AC002535; NID:92529657; PID:92529671

Query Match 34.0%; Score 99.5; DB 2; Length 206;
Best Local Similarity 36.0%; Pred. No. 0.00014; Matches 18; Conservative 8; Mismatches 19; Indels 5; Gaps 2; Db 157 CSICLESLVSGPKPRDVTMTCSSHVFHNGCLLWLR--KNTCPLCRTE 204

RESULT 28

G84530 probable RING-H2 zinc finger protein [imported] - Arabidopsis thaliana
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84530
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: G84530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-204 <STO>
A;Cross-references: GB:AE002093; NID:94335724; PIDN:AD17402.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g15580
A;Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 204;
Best Local Similarity 36.2%; Pred. No. 0.00021; Matches 17; Conservative 6; Mismatches 22; Indels 2; Gaps 1; Db 158 CAICIDRFFKGETLWHLPCAHKFHSICLLFWLDT--NVCPYCRTDI 202

RESULT 29

E84918 hypothetical protein At2g47700 [imported] - Arabidopsis thaliana
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84918
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: E84918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: GB:AB002093; NID:93738284; PIDN: AAC63626.1; GSPDB:GN00139

C;Genetics: 33.3%; Score 97.5; DB 2; Length 257;
 A;Gene: At2g47700
 A;Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 324;
 Best Local Similarity 41.3%; Pred. No. 0.00032; Mismatches 5;
 Matches 19; Conservative 5; Indels 20; Gaps 2; Gaps 1;

RESULT 30

H96703 Query 4 CTCIC-SDFPDHSRVAATHCAGHTPHLOCLIQWETAPSRTPCQCR 47
 Db 38 CSICLESVLDGTTSKAKLQCGRPHDQIGSATNNKGAMQCPCRCR 83

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: H96703
 C;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 C;Reference number: A86141; MUID:21016719
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-343 <STO>
 A;Cross-references: GB:AE005173; NID:96553869; PIDN:AAF16555.1; GSPDB:GN00141
 A;Genetics:
 A;Gene: T23K23.8
 A;Map position: 1

Query Match 33.4%; Score 98; DB 2; Length 343;
 Best Local Similarity 27.7%; Pred. No. 0.00033; Mismatches 13; Indels 19; Gaps 1;

RESULT 31

T48058 Query 4 CTCSDFDDHSRVAATHCAGHTPHLOCLIQWETAPSRTPCQCR 50
 Db 292 CCCICLSSYEDGAELVSLPONHHFHSTCTVWLKM-NATCPLKFNTI 336

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: T48058
 C;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 C;Reference number: A86141; MUID:21016719
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <STO>
 A;Cross-references: GB:AE005172; NID:98778785; PIDN:AAF79793.1; GSPDB:GN00141
 A;Genetics:
 A;Gene: T32E20.33
 A;Map position: 1

Query Match 33.4%; Score 98; DB 2; Length 343;
 Best Local Similarity 27.7%; Pred. No. 0.00033; Mismatches 13; Indels 19; Gaps 1;

RESULT 32

F86488 Query 1 LSLCTIC-SDFPDHSRVAATHCAGHTPHLOCLIQWETAPSRTPCQCRQV 50
 Db 110 LEECSVCLSEFEDEDEGRVLVLPKCGHVHFDCIDTWRSSS-CPLCRAPV 158

C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: F86488
 C;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 C;Reference number: A86141; MUID:21016719
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <STO>
 A;Cross-references: GB:AE005172; NID:98778785; PIDN:AAF79793.1; GSPDB:GN00141
 A;Genetics:
 A;Gene: T32E20.33
 A;Map position: 1

Query Match 33.1%; Score 97; DB 2; Length 211;
 Best Local Similarity 35.6%; Pred. No. 0.00029; Mismatches 7;
 Matches 16; Conservative 7; Indels 2; Gaps 1; Gaps 1;

RESULT 33

T19328 Query 3 LCTICSDDFDHRSRVAATHCAGHTPHLOCLIQWETAPSRTPCQCR 47
 Db 85 ICCICQDRQRAGVGKLNCGHNFHINSWKWILT-KKQCPVCQ 127

C;Species: hypothetical protein C16C10.7 - Caenorhabditis elegans
 C;Accession: T19328
 C;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 C;Reference number: Z1.9108
 A;Accession: T19328
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-235 <WIL>
 A;Cross-references: EMBL:Z46787; PIDN:CAA86745.1; GSPDB:GN00021; CESP:C16C10.7
 A;Experimental source: clone C16C10
 C;Genetics:
 A;Gene: CESP:C16C10.7
 A;Map position: 3

A;Introns: 23/2; 105/3; 196/1

C;Superfamily: RING finger homology <RRN>
 F;22-72/Domain: RING finger homology <RRN>

Query Match 33.1%; Score 97; DB 2; Length 235;
 Best Local Similarity 40.0%; Pred. No. 0.00032; Mismatches 18;
 Matches 18; Conservative 6; Indels 17; Gaps 4; Gaps 2;

Query Match 33.1%; Score 97; DB 2; Length 235;
 Best Local Similarity 40.0%; Pred. No. 0.00032; Mismatches 18;
 Matches 18; Conservative 6; Indels 17; Gaps 4; Gaps 2;

Query 4 CTCSDFDDHSRVAATHCAGHTPHLOCLIQWETAPSRTPCQCR 47

A; Map position: 1
A; Introns: 3/1; 27/3; 86/1; 154/1; 201/3; 240/3; 268/3; 297/3
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: B96705
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Mazziali, M.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86441; MUID:21016719
A; Accession: B96705
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-145 <STO>
C; Genetics:
A; Cross-references: GB:AE005173; NID:96715736; PIDN:AAF26497.1; GSPDB:GN00141
A; Gene: T22E19.19
A; Map position: 1

Best Local Similarity 31.9%; Pred. No. 0.00062;
Matches 15; Conservative 9; Mismatches 21; Indels 2; Gaps 1;

Qy	4	CTICSDFFDHISRDYA-AIHCGHTFHQLQCLIQWFETAPSRTCPQCRIQV 50
	: :: : : : :	
Db	317	CVTCLEEVYEGTEIRVLPGHERIPKCVDPWL--LSKARCPGLQFDV 361

Search completed: September 4, 2002, 16:13:07
Job time: 3251 sec

RESULT 39
B96705
unknown protein, 88740-88303 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: B96705
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Mazziali, M.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86441; MUID:21016719
A; Accession: B96705
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-145 <STO>
C; Genetics:
A; Cross-references: GB:AE005173; NID:96715736; PIDN:AAF26497.1; GSPDB:GN00141
A; Gene: T22E19.19
A; Map position: 1

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Matches 15; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

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	: :: : : : :	
Db	34	VCATCCKEEFVGEBKGELKLHLYHSSCIVSWLNI-HNTCPICREFV 79

RESULT 40
T26958
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C; Species: *Caenorhabditis elegans*
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C; Accession: T26958
R; Matthews, L.
submitted to the EMBL Data Library, September 1998
A; Reference number: Z20290
A; Accession: T26958
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-377 <WIL>
A; Cross-references: EMBL:AL031635; PIDN:CAB54384.1; GSPDB:GN00021; CESP:Y47D3B.11
A; Experimental source: clone Y47D3B
C; Genetics:
A; Gene: CESP:Y47D3B.11
A; Map position: 3
A; Introns: 52/1; 81/3; 152/3
C; Superfamily: RING finger homology homology <RRN>
F; J13-363/Domain: RING finger homology

Query Match 32.8%; Score 96; DB 2; Length 377;

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